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OM nucleic - nucleic search, using sw model

Run on: June 17, 2003, 18:55:45 ; Search time 2746 Seconds  
(without alignments)  
11053.979 Million cell updates/sec

Title: US-09-807-933B-13

Perfect score: 1043

Sequence: 1 ggatcctgggacaagatgaa.....cgcaagtaaacgaggatcc 1043

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:\*

- 1: gb.ba.\*
- 2: gb.htg.\*
- 3: gb.in.\*
- 4: gb.ov.\*
- 5: gb.pat.\*
- 6: gb.ph.\*
- 7: gb.pl.\*
- 8: gb.pr.\*
- 9: gb.ro.\*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	286.4	27.5	1060	6	A21793 H. insolens
2	286.4	27.5	1060	6	A23635 H. insolens
3	286.4	27.5	1060	6	A23644 H. insolens
4	286.4	27.5	1060	6	A23953 Endoglucana
5	286.4	27.5	1060	6	A23957 Endoglucana
6	286.4	27.5	1060	6	A41658 Sequence 1
7	286.4	27.5	1060	6	A68060 Sequence 55
8	286.4	27.5	1060	6	AR059002 Sequence
9	286.4	27.5	1060	6	AR072921 Sequence
10	286.4	27.5	1060	6	AR163160 Sequence
11	286.4	27.5	1060	6	BD010852 Cellulase
12	286.4	27.5	1060	6	I13884 Sequence 1
13	286.4	27.5	1060	6	I21316 Sequence 1
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16	274.8	26.3	927	6	AR094307 Sequence
17	273.4	26.2	894	6	AR094306 Sequence
18	273.4	26.2	960	6	AR094305 Sequence
19	271.8	26.1	922	6	A68070 Sequence 65
20	271.8	26.1	922	6	AR163167 Sequence
21	268.2	25.7	922	6	A68078 Sequence 73
22	268.2	25.7	922	6	AR163171 Sequence
23	260.2	24.9	1174	6	A92311 Sequence 1
24	260.2	24.9	1174	6	AR075389 Sequence
25	260.2	24.9	1174	6	AR094310 Sequence
26	257.4	24.7	919	6	A68072 Sequence 67
27	257.4	24.7	919	6	AR163168 Sequence
28	246.2	23.6	1132	6	AR094315 Sequence
29	246.2	23.6	913	6	AR094311 Sequence
30	237.8	22.8	885	6	AR094316 Sequence
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34	235.4	22.6	1473	6	A23646 F. oxysporu
35	235.4	22.6	1473	6	A23955 Endoglucana
36	235.4	22.6	1473	6	A23959 Endoglucana
37	235.4	22.6	1473	6	A41660 Sequence 3
38	235.4	22.6	1473	6	AR072922 Sequence
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42	235.4	22.6	1473	6	I21317 Sequence 3
43	235.4	22.6	1473	6	I57984 Sequence 3
44	233	22.3	924	6	A68074 Sequence 69
45	233	22.3	924	6	AR163169 Sequence

ALIGNMENTS

RESULT 1

A21793

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

FEATURES

source

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/strain="DSM 1800"

/db\_xref="taxon:34413"

A21793

H. insolens

A21793

A21793.1

Humicola insolens.

Humicola insolens

Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.

Location/Qualifiers

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/organism="Humicola insolens"

/strain="DSM 1800"

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1060 bp

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linear

PAT 20-SBP-1995

1060 bp

mRNA

linear

PAT 20-SBP-1995

1060 bp

mRNA

linear

PAT 20-SBP-1995

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BASE COUNT 190 a 377 c 288 g 205 t  
ORIGIN

Query Match 27.5%; Score 286.4; DB 6; Length 1060;  
Best Local Similarity 70.7%; Pred. No. 2.5e-35;  
Matches 461; Conservative 0; Mismatches 166; Indels 25; Gaps 5;

381 CAGCGCTGTACGGGTGGCGCTAGCGGC-AACGGCGTCACTACCGCTACTGGGACTGCT 439  
47 CCGCCCTTCTGGCGGTGGCGCTAGCGGC-TGCGGTGATGCGAGGTCCACCGCTACTGGGACTGCT 106  
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977 AGGAGGTCACTTGGCGGTGACCTTGGCGGTGACGCGGTGACGCGGTGACGCGGTGACGCGGTGAC 1028  
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BASE COUNT 190 a 377 c 288 g 205 t  
ORIGIN

Query Match 27.5%; Score 286.4; DB 6; Length 1060;  
Best Local Similarity 70.7%; Pred. No. 2.5e-35;  
Matches 461; Conservative 0; Mismatches 166; Indels 25; Gaps 5;

381 CAGCGCTGTACGGGTGGCGCTAGCGGC-AACGGCGTCACTACCGCTACTGGGACTGCT 439  
47 CCGCCCTTCTGGCGGTGGCGCTAGCGGC-TGCGGTGATGCGAGGTCCACCGCTACTGGGACTGCT 106  
440 GCAAGCGTTCGTGCTGGTGGCGCGGCAAGGCTAAAGTCAAGTCCGCTGCTCAAGTCTGCA 499  
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RESULT 2  
A23635  
LOCUS A23635 1060 bp mRNA linear PAT 23-FEB-1995  
DEFINITION H. insolens endoglucanase gene.  
ACCESSION A23635  
VERSION A23635.1 GI:832886  
KEYWORDS Humicola insolens.  
SOURCE Humicola insolens  
ORGANISM Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.



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Qy	857	CGCGCTACGCGGCGCATCAGCTCCGCGAGCGATGTCTGTCCTTCCCGAGCGCCTCCAGG	916
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DEFINITION	Sequence 1 from Patent EP0633311.
ACCESSION	A41658
VERSION	A41658.1
KEYWORDS	GI:2297284
SOURCE	unidentified.
ORGANISM	unidentified
REFERENCE	unclassified.
AUTHORS	1 (bases 1 to 1060)
TITLE	Herbots,I.M. and Jansen,M.P.
JOURNAL	Hydrophobic amines for cellulase stabilization in liquid detergent
COMMENT	compositions containing anionic surfactant and cellulase
FEATURES	Patent: EP 0633311-A 1 11-JAN-1995;
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Qy	381	CAGCGCTGT	CAGCGGTGGCGCTAGCGGC	AACGGCGTCACTACCGGCTACTGGGACTGCT	439
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DEFINITION Sequence 55 from Patent W09743409.  
ACCESSION A68060  
VERSION A68060.1 GI:4756862  
KEYWORDS Humicola insolens.  
SOURCE Humicola insolens.  
ORGANISM Humicola insolens.  
REFERENCE 1 (bases 1 to 1060)  
AUTHORS Dalboe, H., Diderichsen, B., Sandal, T. and Kauppinen, S.  
TITLE METHOD OF PROVIDING NOVEL DNA SEQUENCES  
JOURNAL Patent: WO 9743409-A 55 20-NOV-1997;  
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Query Match 27.5%; Score 286.4; DB 6; Length 1060;  
Best Local Similarity 70.7%; Pred. No. 2.5e-35;  
Matches 461; Conservative 0; Mismatches 166; Indels 25; Gaps 5;  
Qy 381 CAGCGCTGTGAGCGGTGGCGCTAGCGGC-AACGCGGTCACTACCGGCTACTGGGACTGCT 439

Db 47 CGCGCTGCGCGTGTGGCCCTTGGCGCTGATGGCAGGTCCACCGCTACTGGGACTGCT 106  
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Db 107 GCAAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 166  
Qy 500 ACAAGGACGCGCTCAACCGCTTCTAGGAGCTTCCAAAGCCAGTCCGGCTGCA--CGCG 556  
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RESULT 8  
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DEFINITION Sequence 7 from patent US 5837847.  
ACCESSION AR059002  
VERSION AR059002.1 GI:5984579  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1060)  
AUTHORS Roper, J.C., Moyer, D.L., Wendy, V.T. and Shuster, J.R.  
TITLE Non-toxic, non-toxicogenic, non-pathogenic fusarium expression system  
JOURNAL Patent: US 5837847-A 7 17-NOV-1998;  
FEATURES Location/Qualifiers  
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BASE COUNT 190 a 377 c 288 g 205 t  
ORIGIN  
Query Match 27.5%; Score 286.4; DB 6; Length 1060;  
Best Local Similarity 70.7%; Pred. No. 2.5e-35;  
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Qy 381 CAGCGCTGTGAGCGGTGGCGCTAGCGGC-AACGCGGTCACTACCGGCTACTGGGACTGCT 439  
Db 47 CGCGCTGCGCGTGTGGCCCTTGGCGCTGATGGCAGGTCCACCGCTACTGGGACTGCT 106

440 GGAAGGCTTCCTGCTCGTGGCCCGGCAAGCTAACTCAGCTCGCTCTGCTCAAGTCTGCA 499  
107 GCAAGCTTCCTGCTCGTGGCCCGGCAAGAGCTCCCGTGAACAGCTGCTCTTTCTGCA 166  
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677 AGCTCACCTTCACCTCCACAGCGTGTGTGGCAAGAGATGGTGTGCTCAGGTCAACACA 736  
344 AGCTCACCTTCACATCCGGTCTGTGTGGCAAGAGATGGTGTGCTCAGGTCAACACA 403  
737 CTGGCGGTGACCTTGGGAGCTCGACCGGTGCGGCTTCGATCTCAGATGCCCGGGCGG 796  
404 CTGGCGGTGATCTTGGAGCAA-----CCACTTCGATCTCAACATCCCGGGCGG 454  
797 GCGTCGCGATCTTCAACGGATGCTGCTCCAGTGGGCGGCTCCCAACGAGCGTGGGGCT 856  
455 GCGTCGCGATCTTCAGCGATGCACTCCCGAGTTCGGGGTCTGCCC-----GGCC 505  
857 CGGCTACGGCGGATCAGTTCGCCAGCGAGTCTGCTGCTCCCGAGCGGCTTCAGG 916  
506 AGCGCTACGGCGGATCTGCTCCGCAACGAGTTCGATGCTCCCGAGCGGCTTCAGG 565  
917 CGGCTACGAGTGGGCTTCAACTGTTCAAGAACCGCGCAACCGCTCCATGACCTACA 976  
566 CGGCTGCTACTGGCGCTTCAGTGTTCAGAACCGCGCAATCCGAGTTCAGCTTCC 625  
977 AGGAGTCACTGCGCCCAAGAGATCACCGCTAAGACCGGATGCTCGCGCAA 1028  
626 GTCAGTCCAGTCCCGCGAGCTCGTCTCGCAGCGGAGTCCCGCGCAA 677

RESULT 9  
AR072921  
LOCUS AR072921 1060 bp DNA linear PAT 28-AUG-2000  
DEFINITION Sequence 1 from patent US 5948672.  
ACCESSION AR072921  
VERSION AR072921.1 GI:9999684  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1060)  
Rasmussen,G., Mikkelsen,J.Moslashedler., Schulein,M.,  
Patkar,S.Anant., Hagen,F., Hjort,C.Malland, and Hestrup,S.  
Cellulase preparation comprising an endoglucanase enzyme  
Patent: US 5948672-A 1 07-SEP-1999;  
Location/Qualifiers  
1..1060  
/organism="unknown"  
BASE COUNT 190 a 377 c 288 g 205 t  
ORIGIN

Query Match 27.5%; Score 286.4; DB 6; Length 1060;  
Best Local Similarity 70.7%; Pred. No. 2.5e-35;  
Matches 461; Conservative 0; Mismatches 166; Indels 25; Gaps 5;  
381 CAGCGCTGTACGGGTGGCGCTAGCGGC-AACGGCGTCACTACCGGCTACTGGGACTGCT 439  
47 CCGCCCTGCGGTGTGGCCCTTGGCGCTGATGGAGGTCCACCGCTACTGGGACTGCT 106  
440 GCAAGGCTTCGCTGCTGCGCGCGGCAAGGCTAACTCAGCTCGCTGTGCAAGTCTGCA 499  
107 GCAAGCTTCGCTGCGGTGGGCAAGAGGCTCCCGTGAACAGGCTGTCTTTCTGCA 166

500 ACAAGGACGGGTCAACCGCTCTTAGCGAGCTCCAAAGCCCGAGTCCGGCTGCAA---CGGCG 556  
167 AC---GCCAATTCAGCGTATCAGCGACTTCAGCGCAAGTCCGGCTGCGAGCCGGCG 223  
557 GCAATCTCATATGTGCAACAGCAACAGCATGGGCTGTCAACAGCAACCTTGTCTAGC 616  
224 GTGTGCGCTACTGTCGCGCGGACAGACCCCATGGGCTGTGAACAGCACTTCGGCTCG 283  
617 GTTTCGCTGCGCTGCCATTAGCGCGGTGGGAGAGCGGCTGTGTGCTGCTCTCTGCTCG 676  
284 GTTTCGCTGCGCACTCTATTGCGCGAGCAATGAGCGGCTGTGTGCTGCGCTGCTAGC 343  
677 AGCTCACCTTCACCTCCACAGCGTGTGTGGCAAGAGATGGTGTGCTCAGGTCAACACA 736  
344 AGCTCACCTTCACATCCGGTCTGTGTGGCAAGAGATGGTGTGCTCAGGTCAACACA 403  
737 CTGGCGGTGACCTTGGGAGCTCGACCGGTGCGGCTTCGATCTCAGATGCCCGGGCGG 796  
404 CTGGCGGTGATCTTGGAGCAA-----CCACTTCGATCTCAACATCCCGGGCGG 454  
797 GCGTCGCGATCTTCAACGGATGCTGCTCCAGTGGGCGGCTCCCAACGAGCGTGGGGCT 856  
455 GCGTCGCGATCTTCAGCGATGCACTCCCGAGTTCGGGGTCTGCCC-----GGCC 505  
857 CGGCTACGGCGGATCAGTTCGCCAGCGAGTCTGCTGCTCCCGAGCGGCTTCAGG 916  
506 AGCGCTACGGCGGATCTGCTCCGCAACGAGTTCGATGCTCCCGAGCGGCTTCAGG 565  
917 CGGCTACGAGTGGGCTTCAACTGTTCAAGAACCGCGCAACCGCTCCATGACCTACA 976  
566 CGGCTGCTACTGGCGCTTCAGTGTTCAGAACCGCGCAATCCGAGTTCAGCTTCC 625  
977 AGGAGTCACTGCGCCCAAGAGATCACCGCTAAGACCGGATGCTCGCGCAA 1028  
626 GTCAGTCCAGTCCCGCGAGCTCGTCTCGCAGCGGAGTCCCGCGCAA 677

RESULT 10  
AR163160  
LOCUS AR163160 1060 bp DNA linear PAT 17-OCT-2001  
DEFINITION Sequence 55 from patent US 6270968.  
ACCESSION AR163160  
VERSION AR163160.1 GI:16233662  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1060)  
Dalb.o elashed,ge.H., Sandal,T., Kauppinen,M.Sakari. and  
Diderichsen,Bslashedrge.  
Method of providing a hybrid polypeptide exhibiting an activity of  
interest  
Patent: US 6270968-A 55 07-AUG-2001;  
Location/Qualifiers  
1..1060  
/organism="unknown"  
BASE COUNT 190 a 377 c 288 g 205 t  
ORIGIN

Query Match 27.5%; Score 286.4; DB 6; Length 1060;  
Best Local Similarity 70.7%; Pred. No. 2.5e-35;  
Matches 461; Conservative 0; Mismatches 166; Indels 25; Gaps 5;  
381 CAGCGCTGTACGGGTGGCGCTAGCGGC-AACGGCGTCACTACCGGCTACTGGGACTGCT 439  
47 CCGCCCTGCGGTGTGGCCCTTGGCGCTGATGGAGGTCCACCGCTACTGGGACTGCT 106  
440 GCAAGGCTTCGCTGCTGCGCGCGGCAAGGCTAACTCAGCTCGCTGTGCAAGTCTGCA 499  
107 GCAAGCTTCGCTGCGGTGGGCAAGAGGCTCCCGTGAACAGGCTGTCTTTCTGCA 166  
500 ACAAGGACGGGTCAACCGCTCTTAGCGAGCTCCAAAGCCCGAGTCCGGCTGCAA---CGGCG 556



Db 167 AC---GCCAATCTCCAGCGTATCAGGACTTCAGCGCAAGTCCGGCTCGAGCGCGGCG 223  
Qy 557 GCACCTCTACATGTGCAAGCAGCAACAGGACATGGGCTGTCAAGCAACACTTGTCTTACG 616  
Db 224 GTGTCCGCTACTCTGTGCGCCGAGCAGACCCATCATGGGCTGTGAACGACGACTTCCGCGTCG 283  
Qy 617 GTTTCTGTCGCGCTGCCATTTAGCGGCGGTGGCAGAGCCGCTGGTGTCTGCTCTCTGCTTCG 676  
Db 284 GTTTTGTGCACTCTATTTCGCGGAGCAATGAGGGGCGCTGTGCTGCGCTGTCTACG 343  
Qy 677 AGCTACCTTCACTCCACAGCGTGTCTGCGAAGAGATGGTGTCTGCTTCCAGGTCAACAA 736  
Db 344 AGCTACCTTCACTCCAGCTGTGCTGCGAAGAGATGGTGTCTGCTTCCAGGTCAACAGCA 403  
Qy 737 CTGCGGCTGACCTTGGGAGCTCGACCGGTGCCACCTTCGATCTCCAGATCCCGGGGCG 796  
Db 404 CTGCGGCTGATCTTGGCAGCAA-----CCACTTCGATCTCAACATCCCGGGGCGG 454  
Qy 797 GCCTCGGCTATCTTCAACGAGTGTCTGCTCCAGTGGGCGCTCCCAACAGCGGCTGGGGCT 856  
Db 455 GCCTCGGCTATCTCGAGGATGACTCCCGAGTTCGGGCTGTGCCC-----GGCC 505  
Qy 857 CGGCTACGCGGCGATCAGCTCCGCGAGCACTGTCTGCTCTCCCGAGCGGCTTCCAGG 916  
Db 506 AGCGCTACGCGGCGATCTCGTCCGCAACAGATGCGATCGGTTCCCGAGCGGCTCAAGC 565  
Qy 917 CGGCTGCAAGTGGCGCTTCACTGCTTCAAGAACCGCGACACCGCTTCCAGCTTACA 976  
Db 566 CGGCTGCTACTGCGGCTTCCGCTGCTTCAAGAACCGCGACATCCGAGCTTCAGCTTCC 625  
Qy 977 AGGAGTCACTGCGCCCAAGAGATCACCGTAAAGACCGGATGCTCGCGCAA 1028  
Db 626 GTGAGTTCAGTCCCGAGCGCTGCTCGTCCAGCGGATGCGCGCGCAA 677

RESULT 11  
BD010852 1060 bp DNA linear PAT 31-JAN-2002  
LOCUS  
DEFINITION  
Cellulase preparation containing endoglucanase.  
BD010852  
ACCESSION  
BD010852.1 GI:18639225  
VERSION  
JP 2001057894-A/1.  
KEYWORDS  
Humicola insolens.  
SOURCE  
Humicola insolens  
ORGANISM  
Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.  
REFERENCE  
1 (bases 1 to 1060)  
Rasmussen,G., Mikkelsen,J.M., Schilein,M., Patkar,S.A., Hagen,F.,  
Miland,H.K. and Hallstopp,S.  
Cellulase preparation containing endoglucanase  
Patent: JP 2001057894-A 1 06-MAR-2001;  
TITLE  
NOVO NORDISK AS  
JOURNAL  
OS Humicola insolens  
COMMENT  
PN JP 2001057894-A/1  
PD 06-MAR-2001  
PF 06-JUL-2000 JP 2000205757  
PR 09-MAY-1990 DK 1159/90, 22-APR-1991 DK 0736/91 PI  
GURETE RASMUSSEN, JAN MOLLER MIKKJELSEN, MARTIN SCHILEIN, PI  
SHANKANT ANANT PATKAR, FRED HAGEN, HJOERT KARSTEN MILAND, PI  
SVEND  
HALLSTOPP  
PC C12N15/09, C12N13/386, C12N11/15, C12N11/19, C12N9/24, D06M16/00// PC  
(C12N15/09, C12R1:77), (C12N15/09, C12R1:645), (C12N9/24, PC  
C12R1:865),  
PC (C12N9/24, C12R1:885), (C12N9/24, C12R1:78), (C12N9/24, C12R1:69),  
PC (C12N9/24, C12R1:685), C12N15/00, (C12N15/00, C12R1:77),  
(C12N15/00, PC C12R1:645)  
CC  
FH Key Location/Qualifiers  
FT mat\_peptide 73..927  
FT sig\_peptide 10..72  
FT CDS 10..927.  
FT Location/Qualifiers  
1..1060  
source

/organism="Humicola insolens"  
/db\_xref="taxon:34413"  
BASE COUNT 190 a 377 c 288 g 205 t  
ORIGIN  
Query Match 27.5%; Score 286.4; DB 6; Length 1060;  
Best Local Similarity 70.7%; Pred. NO. 2.5e-35;  
Matches 461; Conservative 0; Mismatches 166; Indels 25; Gaps 5;  
Qy 381 CAGCGCTGTACGGGTGGGCGCTAGCGGC-AACGGCGTCACTACCCGCTACTGGGACTGCT 439  
Db 47 CGCGCCCTGCGGCTGTGGGCGCTTGGCGCTGATGCGAGGTCCACCCGCTACTTGGGACTGCT 106  
Qy 440 GCAAGGCTTCTGTCTGTGCGCGGCAAGGCTAACTGCTCAGCTCGCTGTCAAGTCTCTGCA 499  
Db 107 GCAAGGCTTCTGTGCGGCTGGGCGCAAGAGGCTCCCGTGAACAGAGCTGTCTTCTCTGCA 166  
Qy 500 ACAAGGAGCGGCTGACCGCTTTAGCGACTTCAACCGCCAGTCCGGCTGCAA---CGGCG 556  
Db 167 AC---GC'AAC'TTCCAGCGTATCAGGACTTTCAGCGCAAGTCCGGCTGCGAGCGGGCG 223  
Qy 557 GCACCTCTTACATGTGCAAGCAGCAACAGGACATGGGCTGTCAAGCAGCAACCTTGTCTTACG 616  
Db 224 GTGTCCGCTTACTCTGTGCGCGGAGCAGACCCATGAGGTGTGAACGAGAGCTTTCGCGCTCG 283  
Qy 617 GTTTCTGCTGCGCTGCTGCAATTAGCGGCGGTGGCGAGAGCGCTGCTGTCTGCTCTGCTTTCG 676  
Db 284 GTTTTGTGCGCACTCTATTTCGCGGAGCAATGAGGGGCGCTGTGCTGCGCTGTCTACG 343  
Qy 677 AGCTACCTTCACTCCACAGCGTGTGCTGGCAAGAGATGGTGTCTGCTTCCAGGTCAACAA 736  
Db 344 AGCTACCTTCACTCCGCTTCTGCTGCTGGCAAGAGATGGTGTCTGCTTCCAGGTCAACAGCA 403  
Qy 737 CTGCGGCTGACCTTGGGAGCTCGACCGGTGCCACCTTCGATCTCCAGATCCCGGGGCG 796  
Db 404 CTGCGGCTGATCTTGGCAGCAA-----CCACTTCGATCTCAACATCCCGGGGCGG 454  
Qy 797 GCCTCGGCTATCTTCAACGAGTGTCTGCTCCAGTGGGCGCTCCCAACAGCGGCTGGGGCT 856  
Db 455 GCCTCGGCTATCTCGAGGATGACTCCCGAGTTCGGGCTGTGCCC-----GGCC 505  
Qy 857 CGGCTACGCGGCGATCAGCTCCGCGAGCACTGTCTGCTCTCCCGAGCGGCTTCCAGG 916  
Db 506 AGCGCTACGCGGCGATCTCGTCCGCAACAGATGCGATCGGTTCCCGAGCGGCTCAAGC 565  
Qy 917 CGGCTGCAAGTGGCGCTTCACTGCTTCAAGAACCGCGACACCGCTTCCAGCTTACA 976  
Db 566 CGGCTGCTACTTGGGCGCTTTCGACTGCTTCAAGAACCGCGACATCCGAGCTTCAGCTTCC 625  
Qy 977 AGGAGTCACTTGCCTCCCAAGGAGATCACCGTAAAGACCGGATGCTCGCGCAA 1028  
Db 626 GTGAGTTCAGTCCCGAGCGCTGCTCGTCCAGCGGATGCGCGCGCAA 677  
RESULT 12  
BD010884  
LOCUS  
DEFINITION  
Sequence 1 from patent US 5443750.  
BD010884  
ACCESSION  
BD010884.1 GI:996364  
VERSION  
KEYWORDS  
SOURCE  
Unknown.  
ORGANISM  
Unclassified.  
REFERENCE  
1 (bases 1 to 1060)  
Convents,A., Busch,A. and Baek,A.C.  
Detergent compositions with high activity cellulase and softening  
TITLE  
Patent: US 5443750-A 1 22-AUG-1995;  
JOURNAL  
Location/Qualifiers  
1..1060  
source  
/organism="unknown"  
BASE COUNT 190 a 377 c 288 g 205 t

## ORIGIN

Query Match 27.5%; Score 286.4; DB 6; Length 1060;  
 Best Local Similarity 70.7%; Pred. No. 2.5e-35;  
 Matches 461; Conservative 0; Mismatches 166; Indels 25; Gaps 5;

QY 381 CAGCGCTGTGAGCGGTGGCGCTAGCGGC-AACGGCGTCACTACCGGCTACTGGGACTGCT 439  
 DB 47 CGCGCTTCCGGGTGTGGCCCTTGGCGCTGATGGCAGGTCCACCGCTACTGGGACTGCT 106

QY 440 GCAAGGCTTCTGCTGCTGGCCCGGCAAGGCTAAGCTCAGCTCGGCTGTCAAGTCTCTGCA 499  
 DB 107 GCAAGGCTTCTGCTGCTGGCCCGGCAAGGCTTCCGCTGAAACAGGCTGTCTTTTCTGCA 166

QY 500 ACAAGGAGCGGCTCAGCGCTCTTAGCGACTCCAAAGCCAGTCCCGGCTGCAA---CGGCG 556  
 DB 167 AC---GCCAACTTCAGCGTATACGGACTTCAGCGCTGAGTCCCGGCTGCAAGGCTGCT 223

QY 557 GCAACTCTTACATGTGCAACGACCAACAGCATGGGCTGTCAACGACAACTTGTCTTACG 616  
 DB 224 GTGTGCGCTACTCTGTGGCGGACAGACCCCATGGCTGTGAACAGGACTTCGCGCTCG 283

QY 617 GTTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 676  
 DB 284 GTTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 343

QY 677 AGCTCACCTTCACTTCCAGCAGCTGTGCTGCAAGAGATGGTCCAGGTCAACAAACA 736  
 DB 344 AGCTCACCTTCACTTCCAGCAGCTGTGCTGCAAGAGATGGTCCAGGTCAACAAACA 403

QY 737 CTGGCGGTGATCTTGGCAGCAA-----CCACTTCGATCTCAACATCCCGCGGCGG 454  
 DB 404 CTGGCGGTGATCTTGGCAGCAA-----CCACTTCGATCTCAACATCCCGCGGCGG 454

QY 797 GCGTGGGATCTTCAACGGATGCTGCTCCAGTGGGCGCTCCCAACGAGCGGTGGGGCT 856  
 DB 455 GCGTGGGATCTTCAACGGATGCTGCTCCAGTGGGCGCTCCCAACGAGCGGTGGGGCT 505

QY 857 CGCGCTACGGCGGATCAGCTCCGCGAGGACTGCTGCTCCCTCCCAAGCGGCTCCAGG 916  
 DB 506 AGCGCTACGGCGGATCAGCTCCGCGAGGACTGCTGCTCCCTCCCAAGCGGCTCCAGG 565

QY 917 CGCGCTCAAGTGGCGCTTCACTGCTTCAAGAGCGGCGGAGGAGGAGGAGGAGGAGGAGG 976  
 DB 566 CGCGCTCAAGTGGCGCTTCACTGCTTCAAGAGCGGCGGAGGAGGAGGAGGAGGAGGAGG 625

QY 977 AGGAGTCACTGCGGCGGAGGATCAGCGCTAAGACCGGATGCTCGCGCAA 1028  
 DB 626 GTGAGTCACTGCGGCGGAGGATCAGCGCTAAGACCGGATGCTCGCGCAA 677

## RESULT 13

121316  
 LOCUS 121316 1060 bp DNA linear PAT 07-OCT-1996  
 DEFINITION Sequence 1 from patent US 5520838.  
 ACCESSION 121316  
 VERSION 121316.1 GI:1601670  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 1060)  
 AUTHORS Baek, A.C., Ceulemans, R.A. and Busch, A.  
 TITLE Compact detergent compositions with high activity cellulase  
 JOURNAL Patent: US 5520838-A 1 28-MAY-1996;  
 FEATURES Location/Qualifiers  
 source 1..1060  
 /organism="unknown"  
 BASE COUNT 190 a 377 c 288 g 205 t  
 ORIGIN

Query Match 27.5%; Score 286.4; DB 6; Length 1060;  
 Best Local Similarity 70.7%; Pred. No. 2.5e-35;

Matches 461; Conservative 0; Mismatches 166; Indels 25; Gaps 5;

QY 381 CAGCGCTGTGAGCGGTGGCGCTAGCGGC-AACGGCGTCACTACCGGCTACTGGGACTGCT 439  
 DB 47 CGCGCTTCCGGGTGTGGCCCTTGGCGCTGATGGCAGGTCCACCGCTACTGGGACTGCT 106

QY 440 GCAAGGCTTCTGCTGCTGGCCCGGCAAGGCTAAGCTCAGCTCGGCTGTCAAGTCTCTGCA 499  
 DB 107 GCAAGGCTTCTGCTGCTGGCCCGGCAAGGCTTCCGCTGAAACAGGCTGTCTTTTCTGCA 166

QY 500 ACAAGGAGCGGCTCAGCGCTCTTAGCGACTCCAAAGCCAGTCCCGGCTGCAA---CGGCG 556  
 DB 167 AC---GCCAACTTCAGCGTATACGGACTTCAGCGCTGAGTCCCGGCTGCAAGGCTGCT 223

QY 557 GCAACTCTTACATGTGCAACGACCAACAGCATGGGCTGTCAACGACAACTTGTCTTACG 616  
 DB 224 GTGTGCGCTACTCTGTGGCGGACAGACCCCATGGCTGTGAACAGGACTTCGCGCTCG 283

QY 617 GTTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 676  
 DB 284 GTTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 343

QY 677 AGCTCACCTTCACTTCCAGCAGCTGTGCTGCAAGAGATGGTCCAGGTCAACAAACA 736  
 DB 344 AGCTCACCTTCACTTCCAGCAGCTGTGCTGCAAGAGATGGTCCAGGTCAACAAACA 403

QY 737 CTGGCGGTGATCTTGGCAGCAA-----CCACTTCGATCTCAACATCCCGCGGCGG 454  
 DB 404 CTGGCGGTGATCTTGGCAGCAA-----CCACTTCGATCTCAACATCCCGCGGCGG 454

QY 797 GCGTGGGATCTTCAACGGATGCTGCTCCAGTGGGCGCTCCCAACGAGCGGTGGGGCT 856  
 DB 455 GCGTGGGATCTTCAACGGATGCTGCTCCAGTGGGCGCTCCCAACGAGCGGTGGGGCT 505

QY 857 CGCGCTACGGCGGATCAGCTCCGCGAGGACTGCTGCTCCCTCCCAAGCGGCTCCAGG 916  
 DB 506 AGCGCTACGGCGGATCAGCTCCGCGAGGACTGCTGCTCCCTCCCAAGCGGCTCCAGG 565

QY 917 CGCGCTCAAGTGGCGCTTCACTGCTTCAAGAGCGGCGGAGGAGGAGGAGGAGGAGGAGG 976  
 DB 566 CGCGCTCAAGTGGCGCTTCACTGCTTCAAGAGCGGCGGAGGAGGAGGAGGAGGAGGAGG 625

QY 977 AGGAGTCACTGCGGCGGAGGATCAGCGCTAAGACCGGATGCTCGCGCAA 1028  
 DB 626 GTGAGTCACTGCGGCGGAGGATCAGCGCTAAGACCGGATGCTCGCGCAA 677

## RESULT 14

157983  
 LOCUS 157983 1060 bp DNA linear PAT 07-OCT-1997  
 DEFINITION Sequence 1 from patent US 5610129.  
 ACCESSION 157983  
 VERSION 157983.1 GI:2483047  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 1060)  
 AUTHORS McCorquodale, F. and Busch, A.  
 TITLE Dye transfer inhibiting compositions  
 JOURNAL Patent: US 5610129-A 1 11-MAR-1997;  
 FEATURES Location/Qualifiers  
 source 1..1060  
 /organism="unknown"  
 BASE COUNT 190 a 377 c 288 g 205 t  
 ORIGIN

Query Match 27.5%; Score 286.4; DB 6; Length 1060;  
 Best Local Similarity 70.7%; Pred. No. 2.5e-35;  
 Matches 461; Conservative 0; Mismatches 166; Indels 25; Gaps 5;

QY 381 CAGCGCTGTGAGCGGTGGCGCTAGCGGC-AACGGCGTCACTACCGGCTACTGGGACTGCT 439

Db 47 CCGCCCTGCGGCTGTGGCCCTTGGCCCTGATGGCAGGTCCACCGCTACTGGGACTGCT 106  
Qy 440 GCAAGGCTTCGCTGCTGGCCGCGCAAGCTTAACGTACGCTCGCTGCTCAAGTCTGCA 499  
Db 107 GCAAGGCTTCGCTGCTGGCCGCGCAAGGCTCCCGTGAACCAAGCTGTCTTTCTGCA 166  
Qy 500 ACAAGGACGCGCTCACCGCTCTTAGCGACTCCAAACGCCAGTCCGGCTGCAA---CGGCG 556  
Db 167 AC---GCCAACTTCACGGCTATACCGACTTCAGCGCAAGTCCGGCTGGAGCGGGCG 223  
Qy 557 GCMACTTCATAGTGTCAAGCAACAGCAGTGGCTGTCAACGAAACCTTGTCTAG 616  
Db 224 GTGTCGCTACTGTCGGCGCAGCAGACCCATGGGCTGTGAACGACGACTTTCGCGCTCG 283  
Qy 617 GTTTCGCTGCGCTGCATTAAGCGGCTGGGAGAGCGGCTGCTGCTCTGCTGCTTCG 676  
Db 284 GTTTCGCTGCGCTGCATTAAGCGGCTGGGAGAGCGGCTGCTGCTGCTGCTGCTGCTAG 343  
Qy 677 AGTCACTTCACCTCCACGAGCGTTCGTCGCAAGAGATGCTGCTCCAGGTCACCAACA 736  
Db 344 AGTCACTTCACATCGGCTCTGTTGCTGGCAAGAGATGCTGCTCCAGTCCACCAACA 403  
Qy 737 CTGGCGGTGACCTTGGGAGCTGACCGGTCGCCACTTCGATCTCCAGATGCCCGCGGCG 796  
Db 404 CTGGCGGTGATCTTGGCAGCA-----CCACTTCGATCTCAACATCCCGCGGCGG 454  
Qy 797 GGTTCGGCATCTCAACGAGTCTGCTCCAGTGGGCGCTCCCAAGCAGCGCTGGGCT 856  
Db 455 GGTTCGGCATCTTCAAGGATGCTGCTCCAGTGGGCGCTCCCAAGCAGCGCTGGGCT 505  
Qy 857 CGGCTACGCGGCGATCAGCTCCCGCAGGAGTCTGCTCCCTCCCGCAGCGGCTCCAGG 916  
Db 506 AGCGCTACGCGGCGATCAGCTCCCGCAGGAGTCTGCTCCCGCAGCGGCTCCAGG 565  
Qy 917 CGGCTGCAAGTGGCGCTTCACTGTTCAAGAACCGCGACACCGCTCCATGACCTACA 976  
Db 566 CGGCTGCTACTGGCGCTTTCGACTGTTCAAGAACCGCGACATCCGAGCTTCAGCTTC 625  
Qy 977 AGGAGTCACTCCGCCAAGGAGATCACCGCTAAGACCGGATGCTCGCGCAA 1028  
Db 626 GTCAGGTCAAGTCCCGCAGGAGCTGCTGCTCGCAGCGGATGCCCGCGAA 677

RESULT 15  
BD002248  
LOCUS 1057 bp DNA linear PAT 31-JAN-2002  
DEFINITION Cellulase preparation comprising endoglucanase.  
ACCESSION BD002248  
VERSION BD002248.1 GI:18630209  
KEYWORDS JP 2000217583-A/1.  
SOURCE Humicola insolens.  
ORGANISM Humicola insolens  
REFERENCE 1 (bases 1 to 1057)  
AUTHORS Gurete,R., Moller,M.J., Martin,S. and Ananto,P.S.  
TITLE Cellulase preparation comprising endoglucanase  
JOURNAL Patent: JP 2000217583-A 1 08-AUG-2000;  
NOVO NORDISK A/S  
OS Humicola insolens  
FN JP 2000217583-A/1  
PD 08-AUG-2000  
PR 22-DEC-1999 JP 1999365341  
PR 09-MAY-1990 DK 1159/90,22-APR-1991 DK 0736/91 PI  
RASMUSSEN GURETE,MIKKJELSEN JAN MOLLER,SCHREIN MARTIN, PI PATKUL  
PC C12N15/09,C11D3/386,C12N1/15,C12N1/19,C12N9/42,C12S3/04, PC  
D06M16/00//  
PC D21H11/20,(C12N9/42,C12R1:645),C12N15/00  
CC  
FH Key Location/Qualifiers  
FT mat\_peptide (73)..(927)  
FT sig\_peptide (10)..(72)  
FT CDS (10)..(927).

FEATURES  
Source  
Location/Qualifiers  
1..1057  
/organism="Humicola insolens"  
/db\_xref="taxon:34413"  
BASE COUNT 190 a 375 c 287 g 205 t  
ORIGIN  
Query Match 27.4%; Score 286; DB 6; Length 1057;  
Best Local Similarity 70.8%; Pred No. 2.9e-35;  
Matches 460; Conservative 0; Mismatches 165; Indels 25; Gaps 5;  
Qy 383 GCGCTGTACGCGTGGCGCTACGGC-AACGGCGTCACTACCGCTACTGGGACTGCTGC 441  
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Qy 442 AAGGCTTGTGTGCTGGCGCGGCAAGCTAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 501  
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Qy 502 AAGGAGCGCGTCAACCGCTCTTAGCGACTCCAAACGCGCAGTCCGGCTGCAA---CGGCGC 558  
Db 166 ---GCCAACTTCAGGCTATCAGGACTTCGACGCGCAAGTCCGGCTGCGAGCGGCGGT 222  
Qy 559 AACTCTCATGTGCAACGACAAACGAGCCATGGGCTGTCAACGACAAACCTTGTCTACGT 618  
Db 223 GTGCGCTACTGTCGCGCGACAGACCCCATGGCTGTGAACGAGACTTCGCGCTCGGT 282  
Qy 619 TTGCGTGTGCTGCTGATTAAGCGCGGTGGCGAGAGCGGCTGTGCTGCTGCTGCTGCTG 678  
Db 283 TTTGTGTCACCTCTATTGTCGCGGAGCAATAGGCGGGCTGGTGTGCTGCGCTGCTACGAG 342  
Qy 679 CTCACCTTCACCTCCACCGAGCGTTCGTCGCAAGAGATGCTGTCAGGTCAACCAACT 738  
Db 343 CTCACCTTCACATCGGCTCTGTTGTCGCAAGAGATGCTGTCAGTTCACCGACT 402  
Qy 739 GCGCGTGAACCTTTGGGAGCTCGACCGGTGCCACTTCGATCTCCAGATGCCCGCGCGCGC 798  
Db 403 GCGCGTGAATCTTTGGGAGCAA-----CCACTTCGATCTCAACATCCCGCGCGCGC 453  
Qy 799 GTGCGCATCTTCAACGAGTGTCTGTCGCGAGTGGGCGCTCCCAACGAGCGGTGGGCTCG 858  
Db 454 GTGCGCATCTTCGAGCGATGCACTCCCGAGTTTCGCGGCTGCGCC-----GGCCAG 504  
Qy 859 CGCTACGCGGCGATCAGCTCCCGCAGCGACTGCTGCTCCCTCCCGAGCGGCTCCAGGCG 918  
Db 505 CGCTACGCGGCGATCTGCTCCCGCAGCGAGTGGATCGGTTCCCGAGCGGCTCCAGCGC 564  
Qy 919 GGTGCAAGTGGCGCTTCAACTGGTTCAAGAAACCGCGCAACCGCTCCATGACCTCAAG 978  
Db 565 GGTGCTACTGCGCGCTTCGACTGGTTCAAGAAACCGCGCAACCTCCGAGCTTCAGCTTC 624  
Qy 979 GAGGTCACTGCGCGCGCGAGGATCACCGCTAAGACCGGATGCTCGCGCAA 1028  
Db 625 CAGGTTCAGTGGCGCGCGAGCTCGTTCGCTCGCAGCGGATGCGCGCGCAA 674

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